1/19

FIGURES

FIG. 1

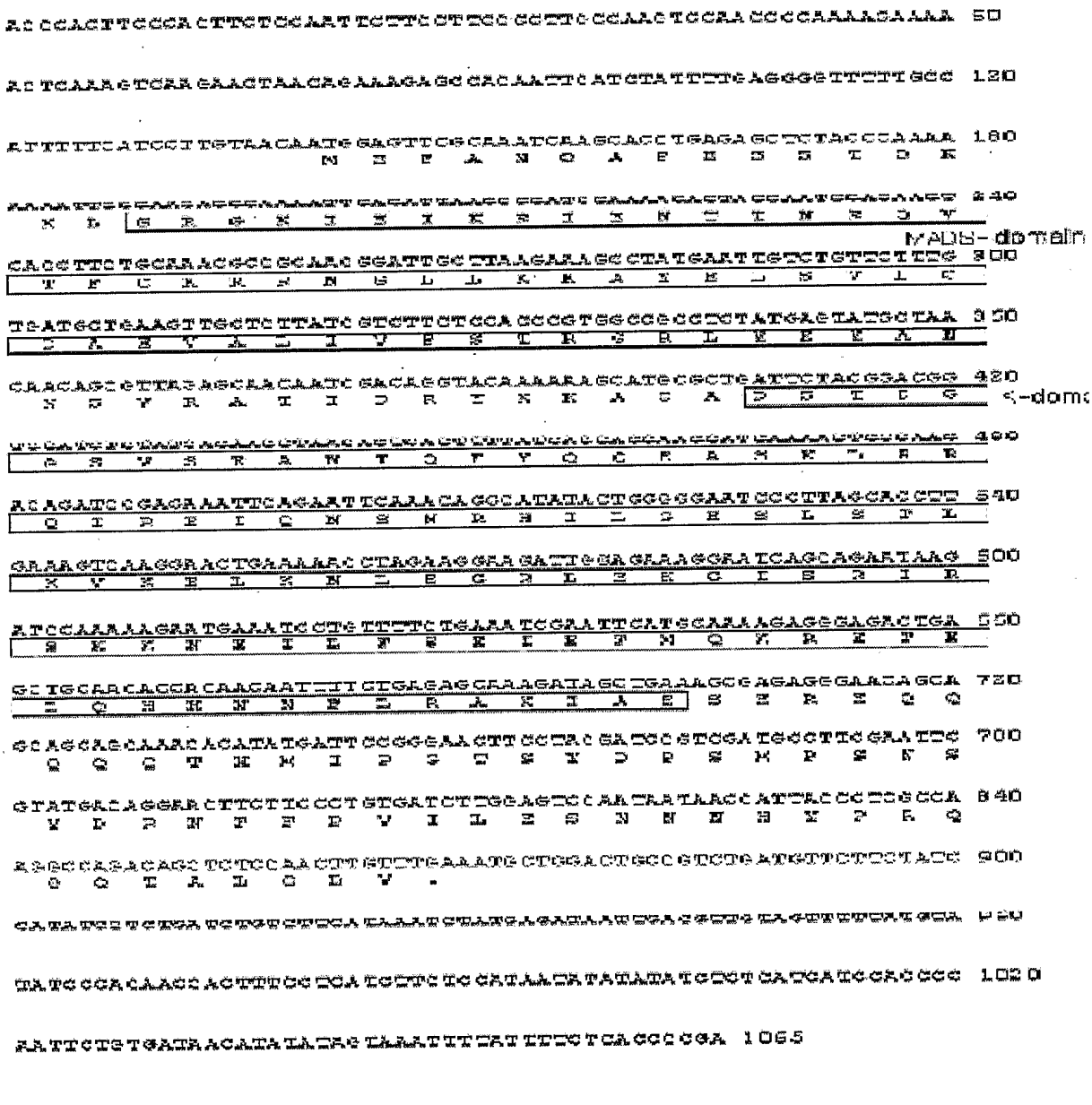

FIG. 2

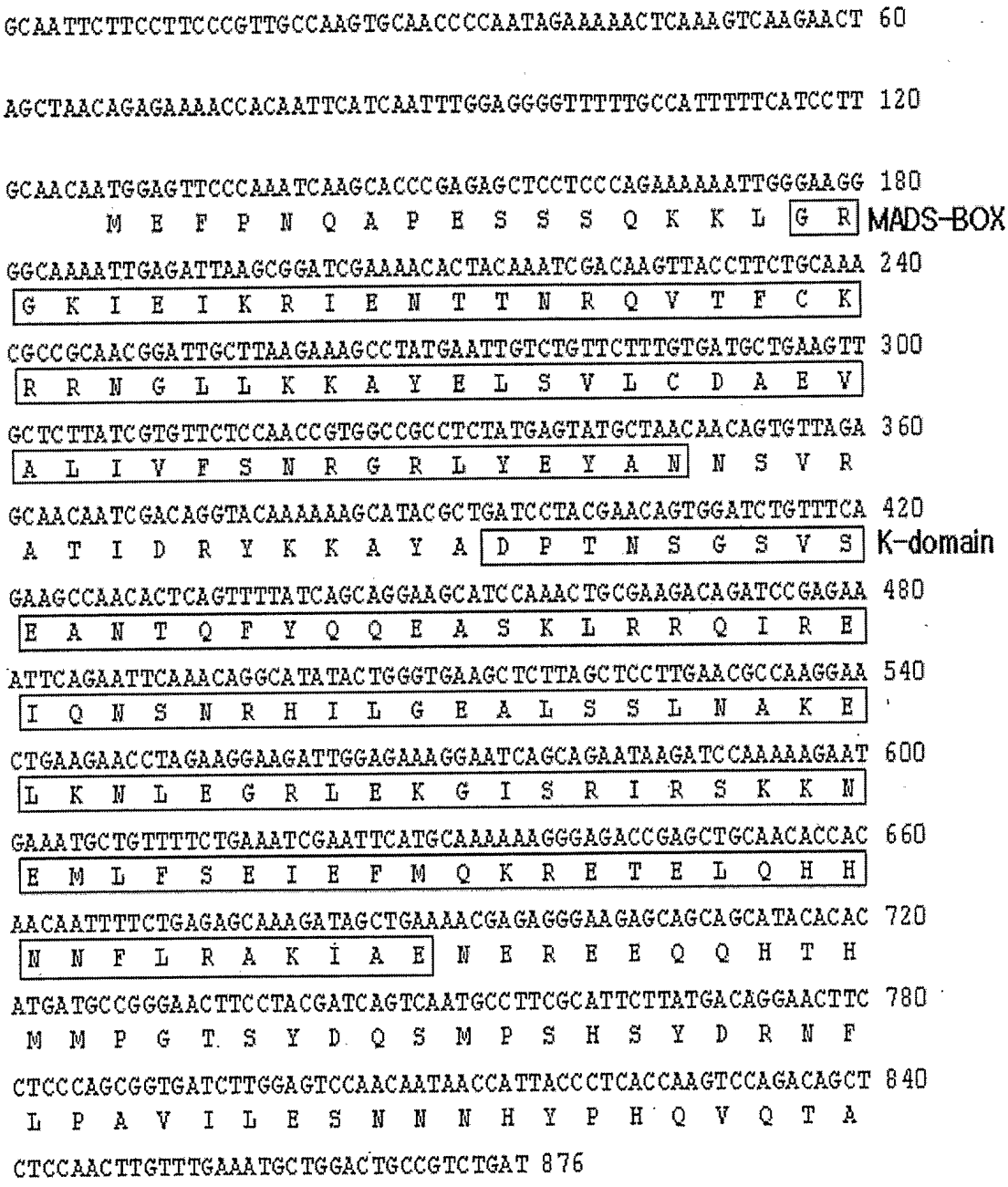
GCAATTCTTCCTTCCCGTTGCCAAGTGCAACCCCAATAGAAAAACTCAAAGTCAAGAACT 60
AGCTAACAGAGAAAACCACAATTCATCAATTTGGAGGGGTTTTTGCCATTTTTCATCCTT 120
GCAACAATGGAGTTCCCAAATCAAGCACCCGAGAGCTCCTCCCAGAAAAAATTGGGAAGG 180
M E F P N Q A P E S S S Q K K L G R
MADS-BOX
GGCAAAATTGAGATTAAGCGGATCGAAAACACTACAAATCGACAAGTTACCTTCTGCAAA 240
G K I E I K R I E N T T N R Q V T F C K
CGCCGCAACGGATTGCTTAAGAAAGCCTATGAATTGTCTGTTCTTTGTGATGCTGAAGTT 300
R R N G L L K K A Y E L S V L C D A E V
GCTCTTATCGTGTTCTCCAACCGTGGCCGCCTCTATGAGTATGCTAACAACAGTGTTAGA 360
A L I V F S N R G R L Y E Y A N N S V R
GCAACAATCGACAGGTACAAAAAAGCATACGCTGATCCTACGAACAGTGGATCTGTTTCA 420
A T I D R Y K K A Y A D P T N S G S V S
K-domain
GAAGCCAACACTCAGTTTTATCAGCAGGAAGCATCCAAACTGCGAAGACAGATCCGAGAA 480
E A N T Q F Y Q Q E A S K L R R Q I R E
ATTCAGAATTCAAACAGGCATATACTGGGTGAAGCTCTTAGCTCCTTGAACGCCAAGGAA 540
I Q N S N R H I L G E A L S S L N A K E
CTGAAGAACCTAGAAGGAAGATTGGAGAAAGGAATCAGCAGAATAAGATCCAAAAAGAAT 600
L K N L E G R L E K G I S R I R S K K N
GAAATGCTGTTTTCTGAAATCGAATTCATGCAAAAAAGGGAGACCGAGCTGCAACACCAC 660
E M L F S E I E F M Q K R E T E L Q H H
AACAATTTTCTGAGAGCAAAGATAGCTGAAAACGAGAGGGAAGAGCAGCAGCATACACAC 720
N N F L R A K I A E N E R E E Q Q H T H
ATGATGCCGGGAACTTCCTACGATCAGTCAATGCCTTCGCATTCTTATGACAGGAACTTC 780
M M P G T S Y D Q S M P S H S Y D R N F
CTCCCAGCGGTGATCTTGGAGTCCAACAATAACCATTACCCTCACCAAGTCCAGACAGCT 840
L P A V I L E S N N N H Y P H Q V Q T A
CTCCAACTTGTTTGAAATGCTGGACTGCCGTCTGAT 876
L Q L V .

FIG. 3

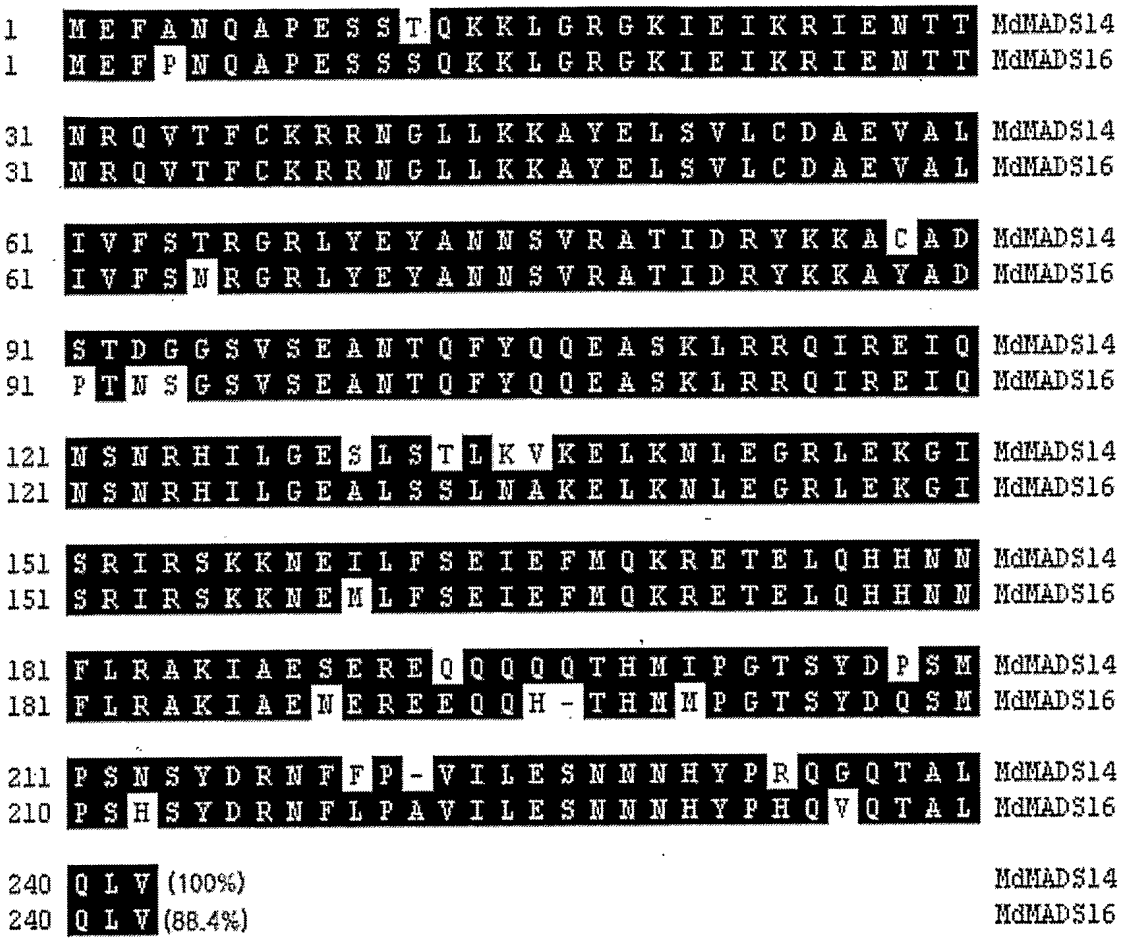
1 MEFANQAPESSTQKKLGRGKIEIKRIENTT MdMADS14
1 MEFPNQAPESSSQKKLGRGKIEIKRIENTT MdMADS16
31 NRQVTFCKRRNGLLKKAYELSVLCDAEVAL MdMADS14
31 NRQVTFCKRRNGLLKKAYELSVLCDAEVAL MdMADS16
61 IVFSTRGRLYEYANNSVRATIDRYKKACAD MdMADS14
61 IVFSNRGRLYEYANNSVRATIDRYKKAYAD MdMADS16
91 STDGGSVSEANTQFYQQEASKLRRQIREIQ MdMADS14
91 PTNSGSVSEANTQFYQQEASKLRRQIREIQ MdMADS16
121 NSNRHILGESLSTLKVKELKNLEGRLEKGI MdMADS14
121 NSNRHILGEALSSLNAKELKNLEGRLEKGI MdMADS16
151 SRIRSKKNEILFSEIEFMQKRETELQHHNN MdMADS14
151 SRIRSKKNEMLFSEIEFMQKRETELQHHNN MdMADS16
181 FLRAKIAESEREQQQQQTHMIPGTSYDPSM MdMADS14
181 FLRAKIAENEREEQQH-THMMPGTSYDQSM MdMADS16
211 PSNSYDRNFFP-VILESNNNHYPRQGQTAL MdMADS14
210 PSHSYDRNFLPAVILESNNNHYPHQVQTAL MdMADS16
240 QLV (100%) MdMADS14
240 QLV (88.4%) MdMADS16

FIG.4

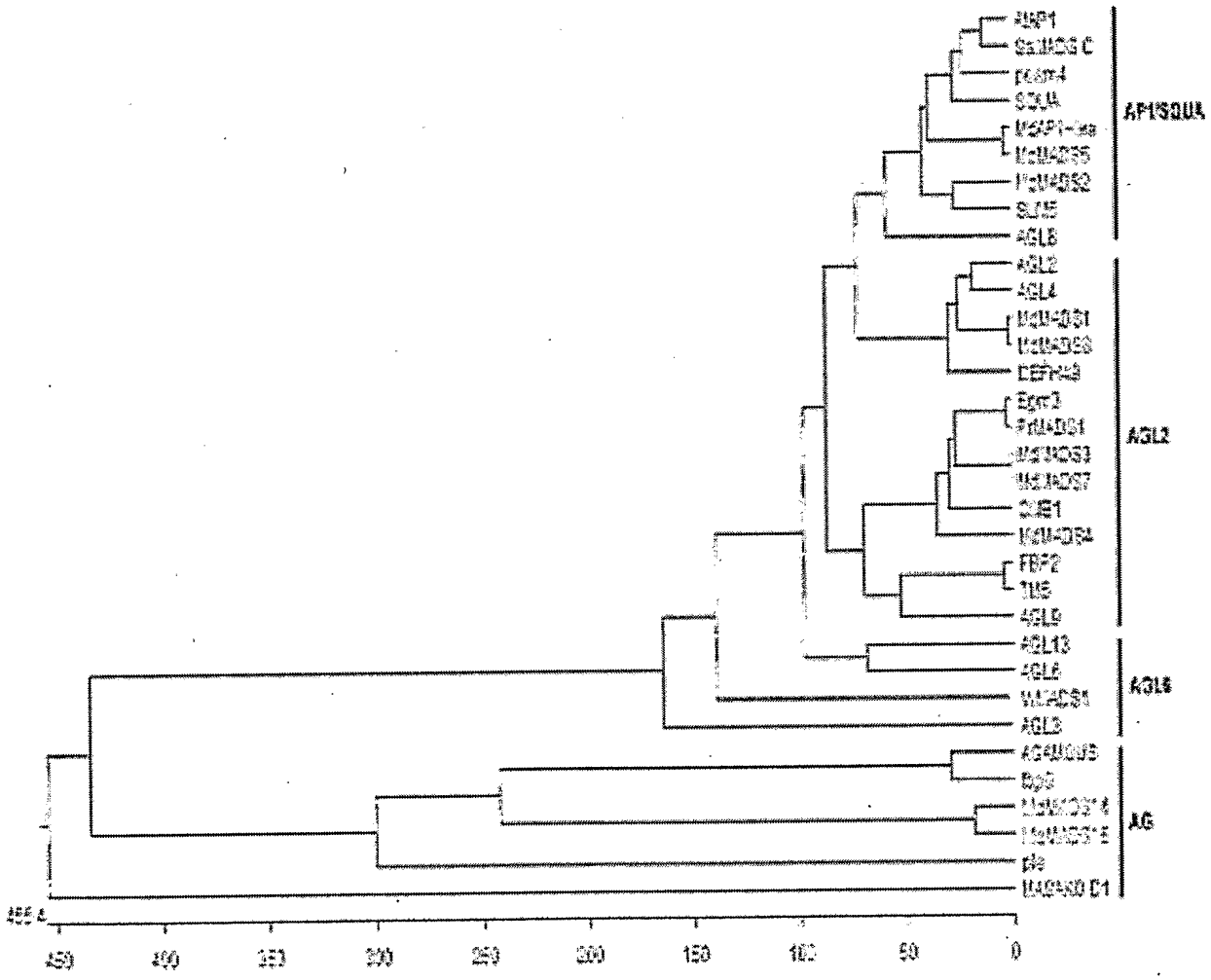

FIG. 5

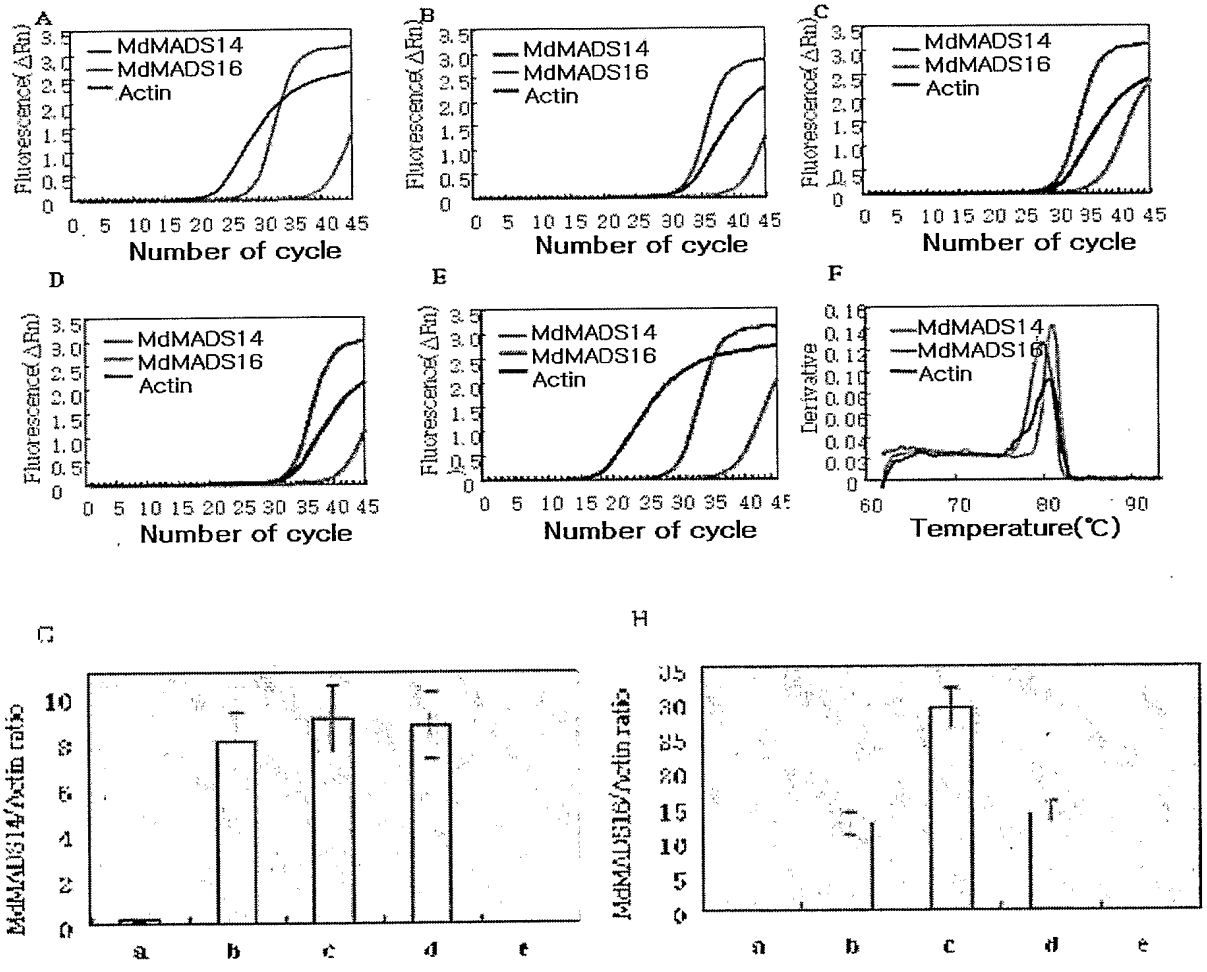
A
B
C
D
E
F
G
H
MdMADS14
MdMADS16
Actin
Fluorescence(ΔRn)
Number of cycle
Derivative
Temperature(℃)
MdMADS14/Actin ratio
MdMADS16/Actin ratio
a
b
c
d
e

FIG. 6

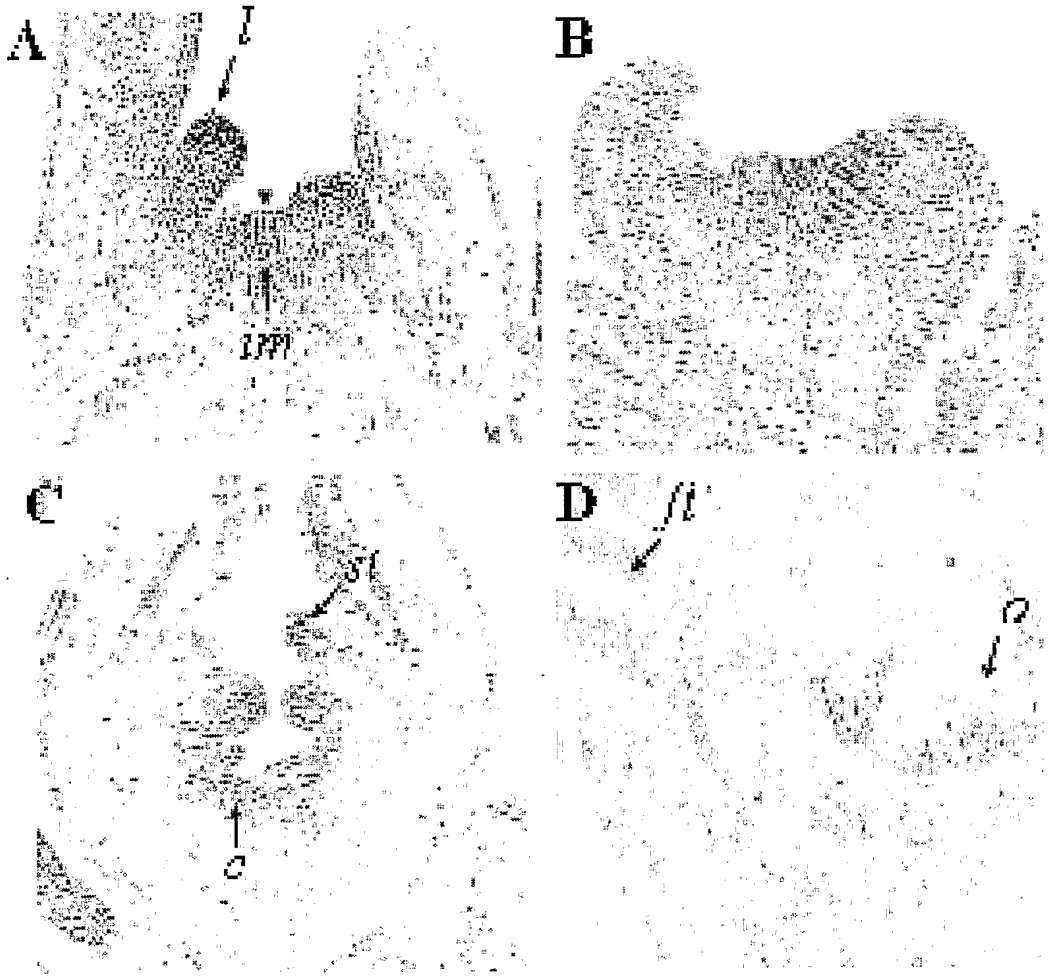

FIG. 7

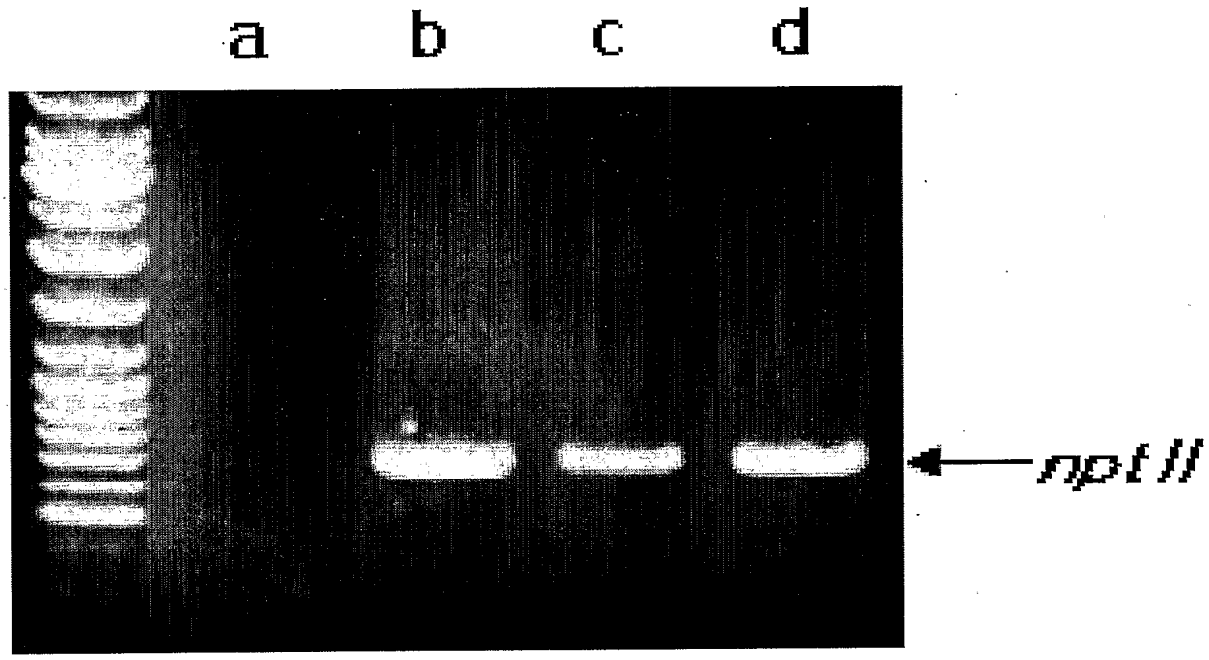

FIG. 8

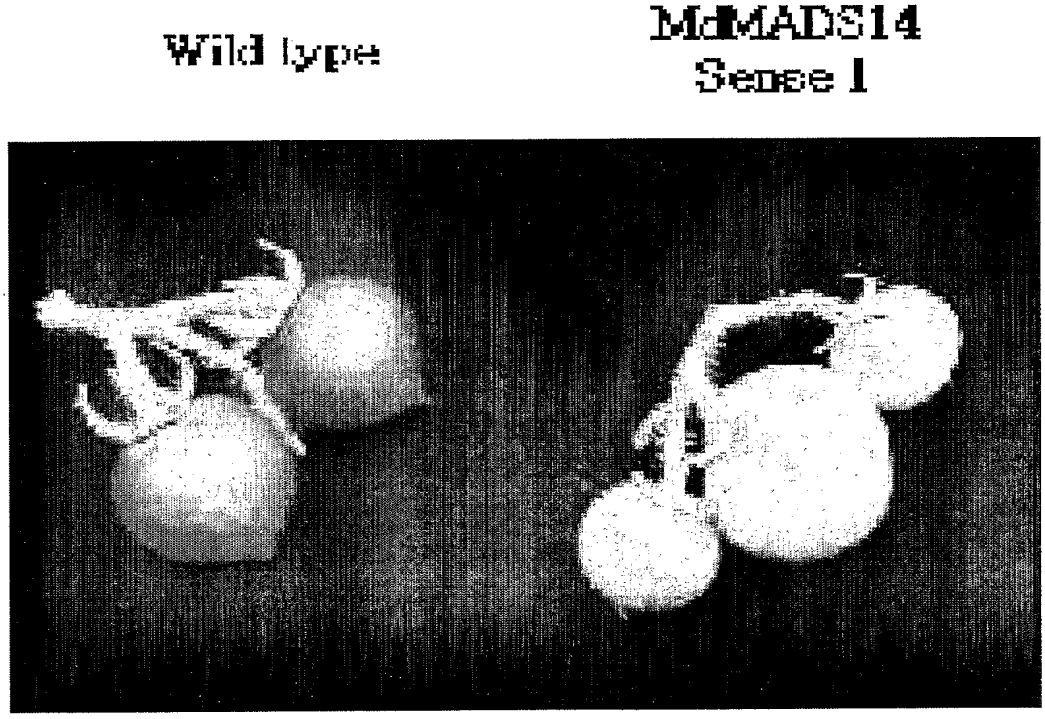

FIG. 9

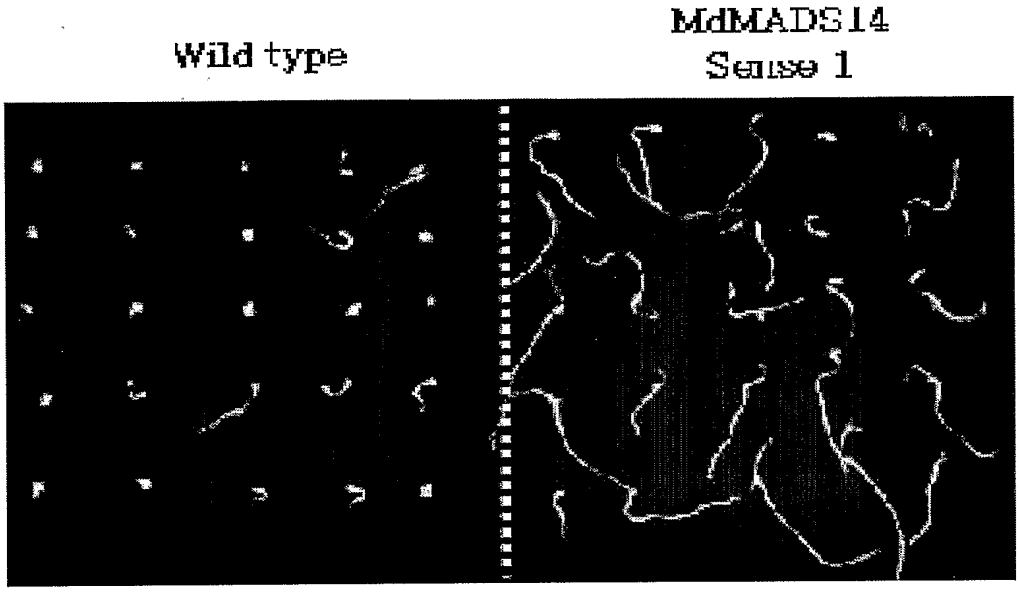

FIG. 10

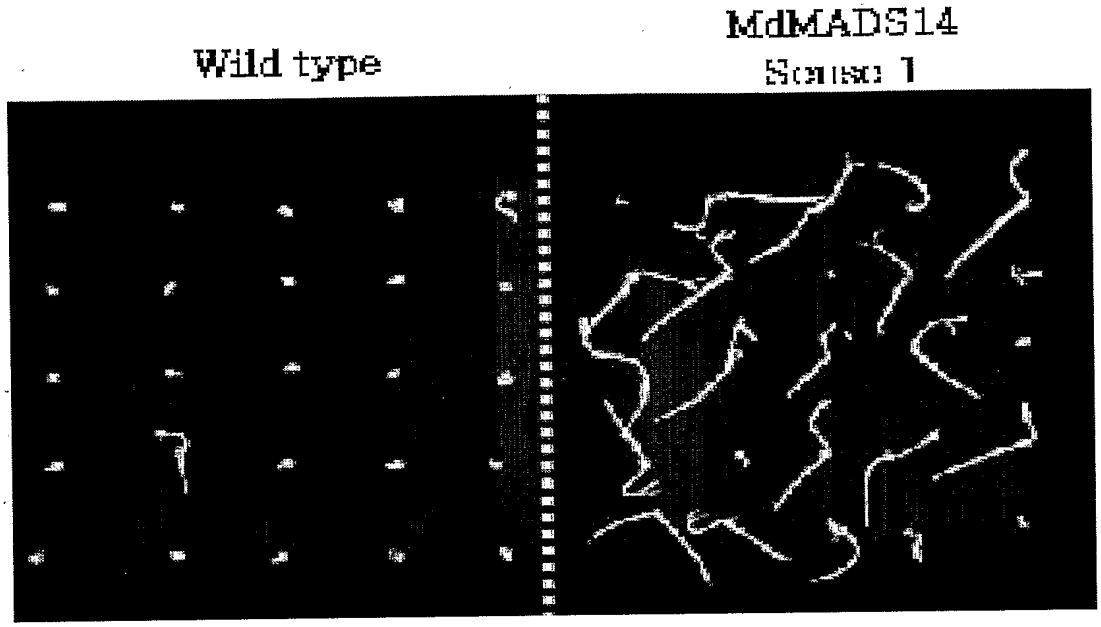

FIG. 11

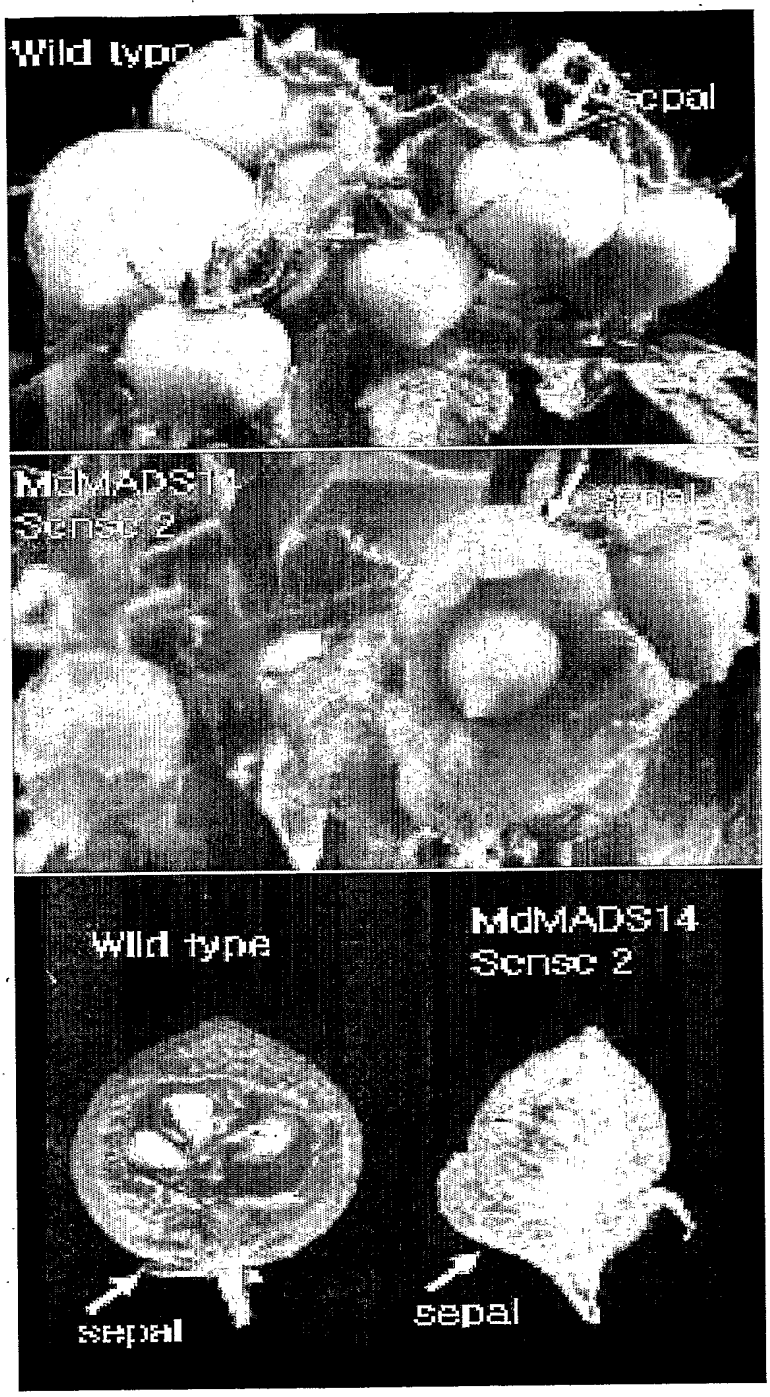
Wild type
sepal
MdMADS14
Scnsc 2
sepal
Wild type
MdMADS14
Scnsc 2
sepal
sepal

FIG. 12

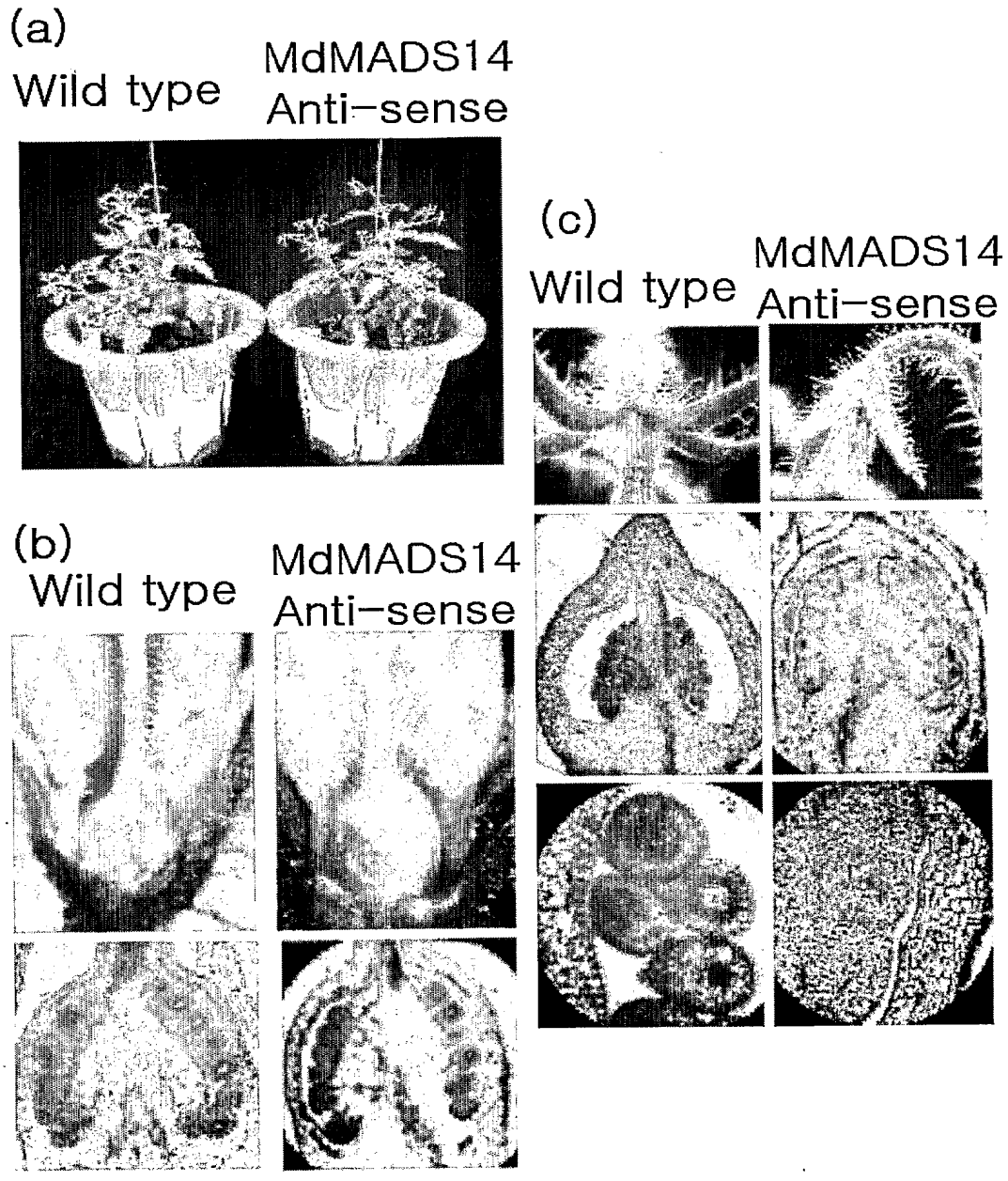
(a)
Wild type
MdMADS14
Anti-sense
(b)
Wild type
MdMADS14
Anti-sense
(c)
Wild type
MdMADS14
Anti-sense

FIG. 13

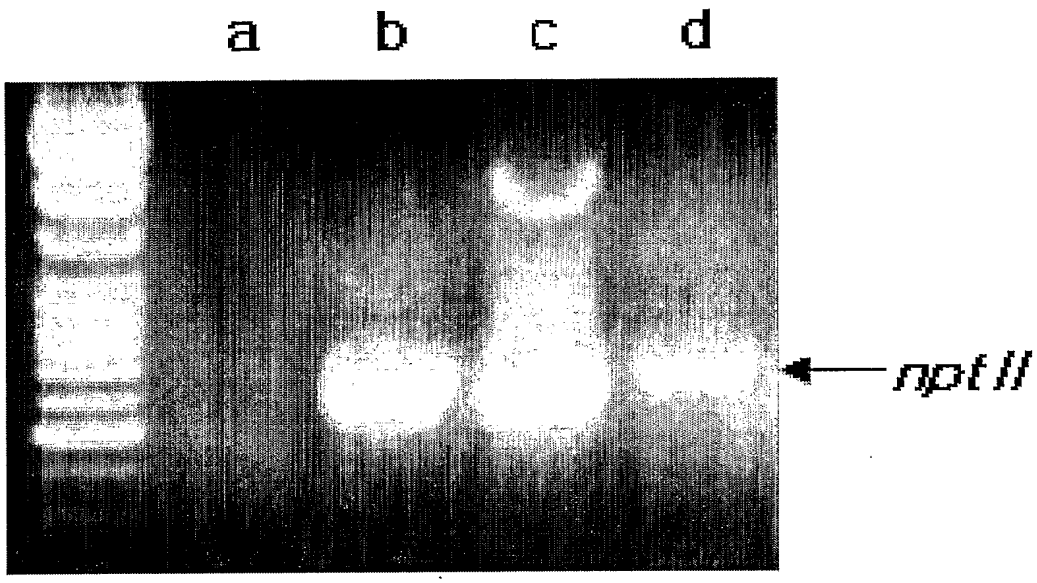

FIG. 14

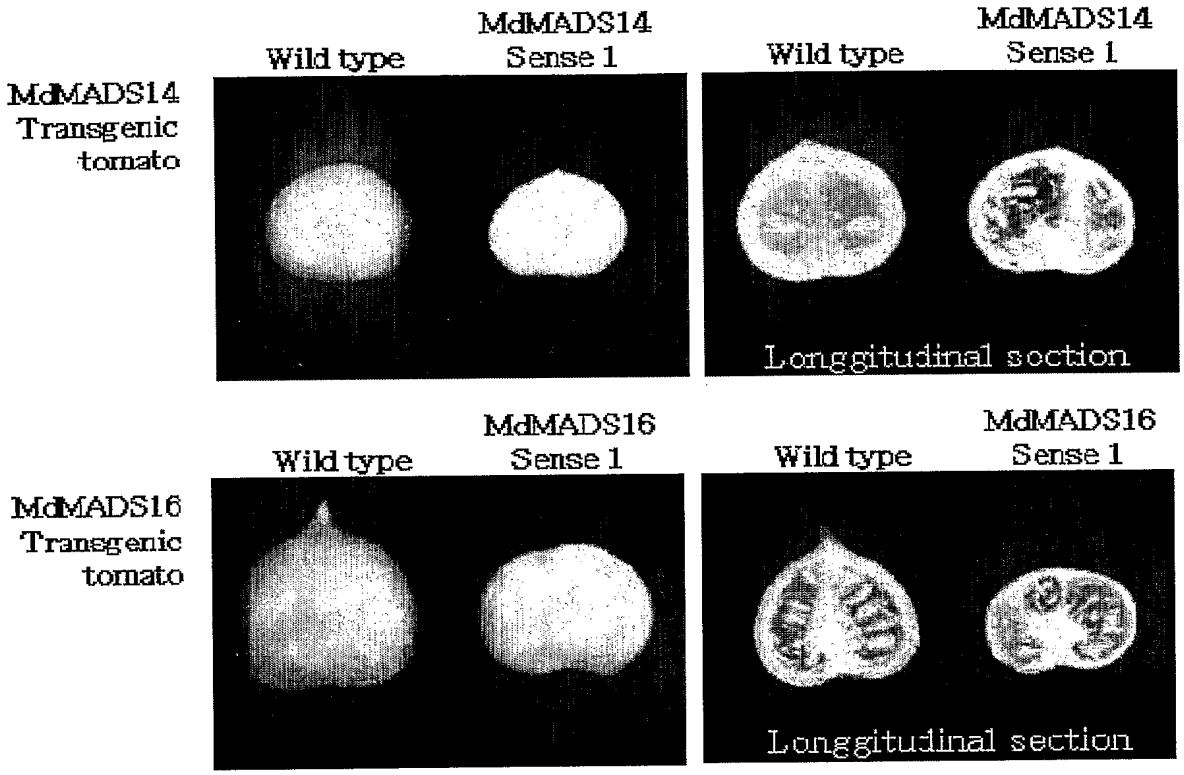
MdMADS14
Transgenic
tomato
Wild type
MdMADS14
Sense 1
Wild type
MdMADS14
Sense 1
Longgitudinal section
MdMADS16
Transgenic
tomato
Wild type
MdMADS16
Sense 1
Wild type
MdMADS16
Sense 1
Longgitudinal section

FIG. 15

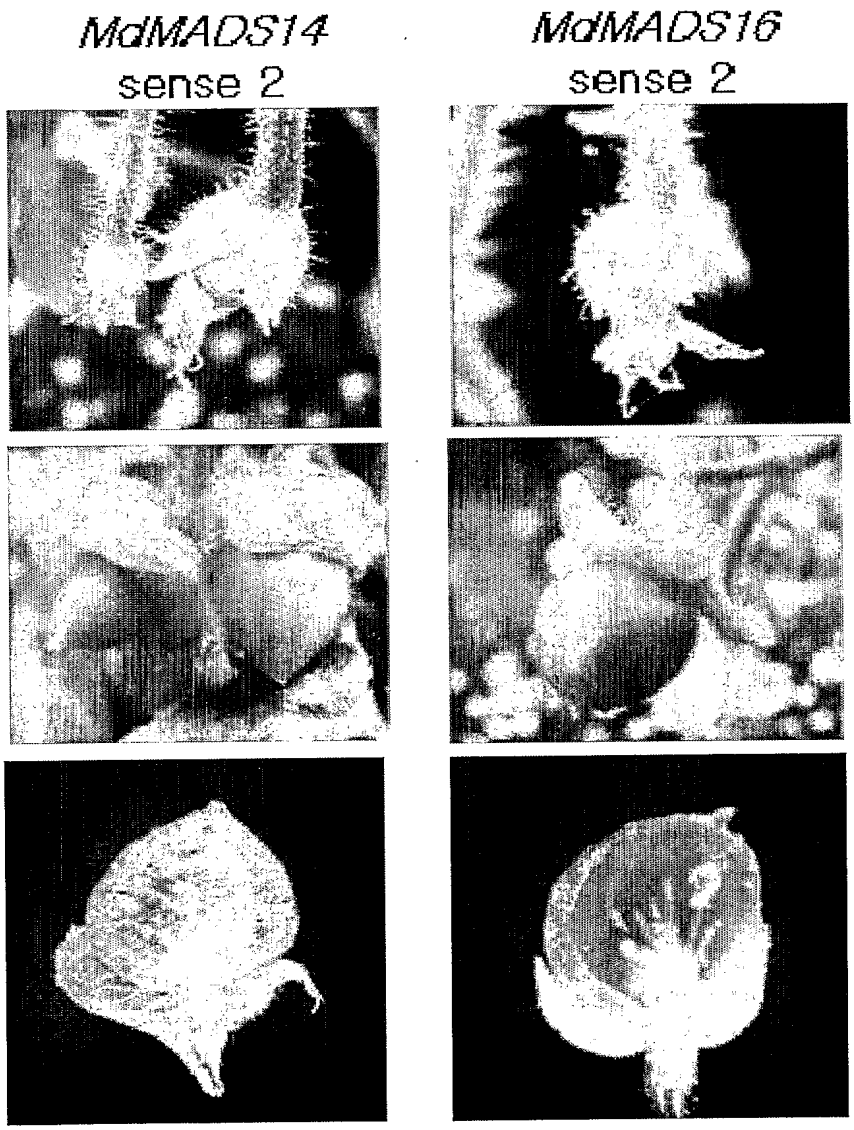

FIG. 16

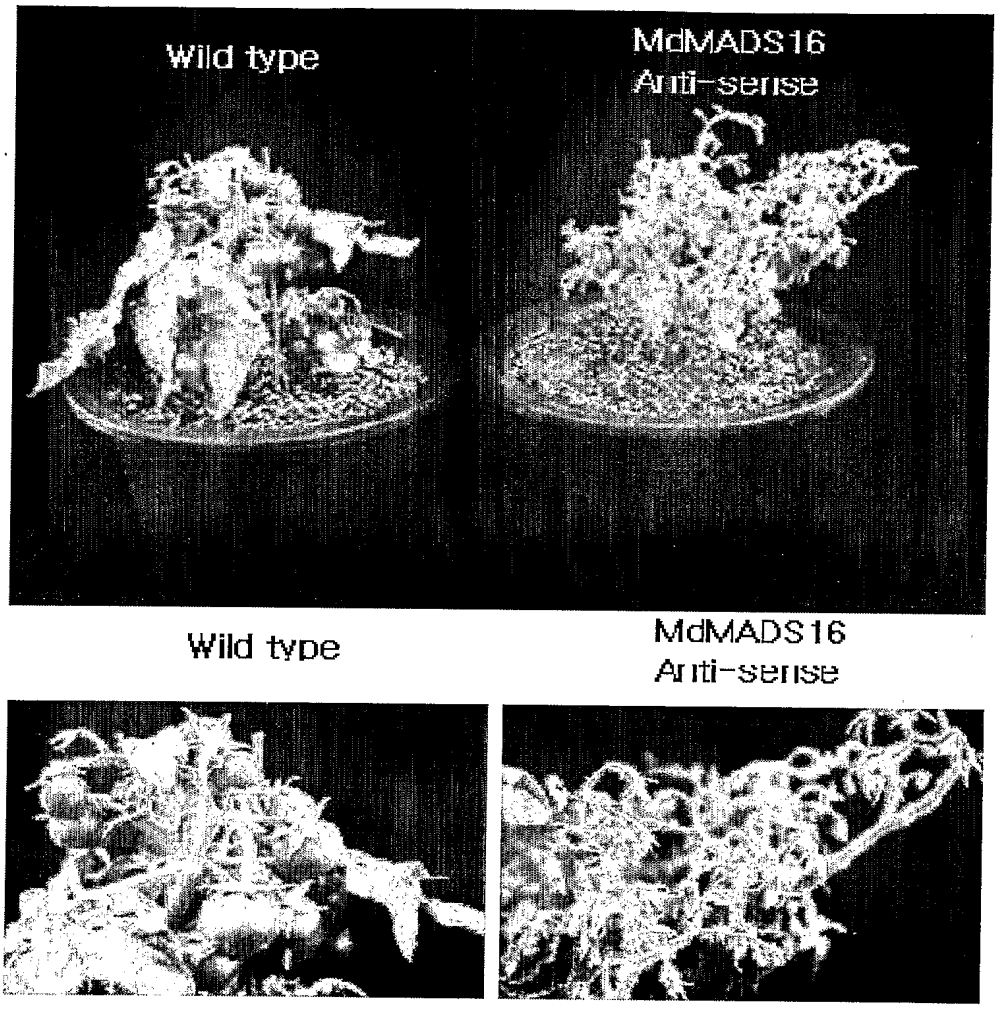
Wild type
MdMADS16
Anti-sense
Wild type
MdMADS16
Anti-sense

FIG. 17

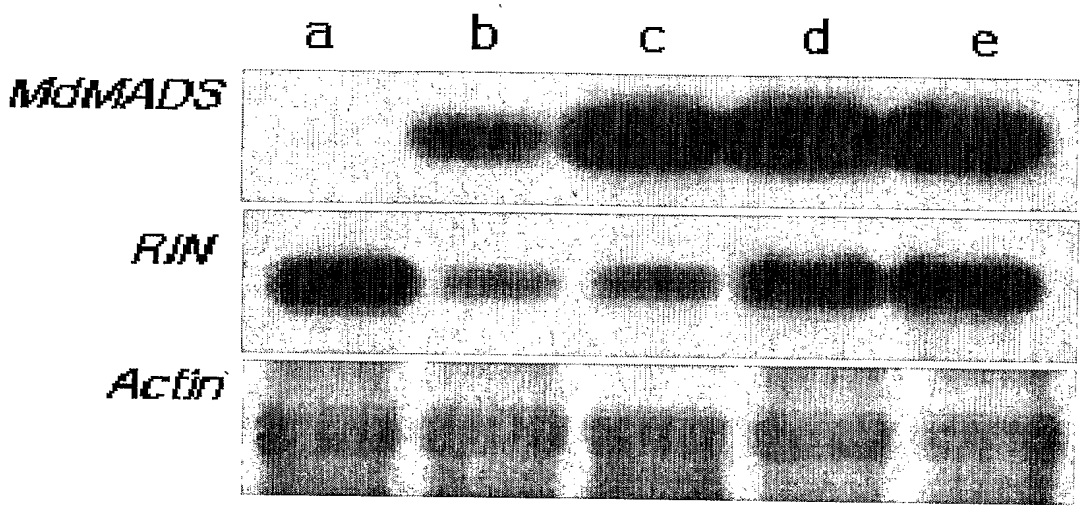

FIG. 18

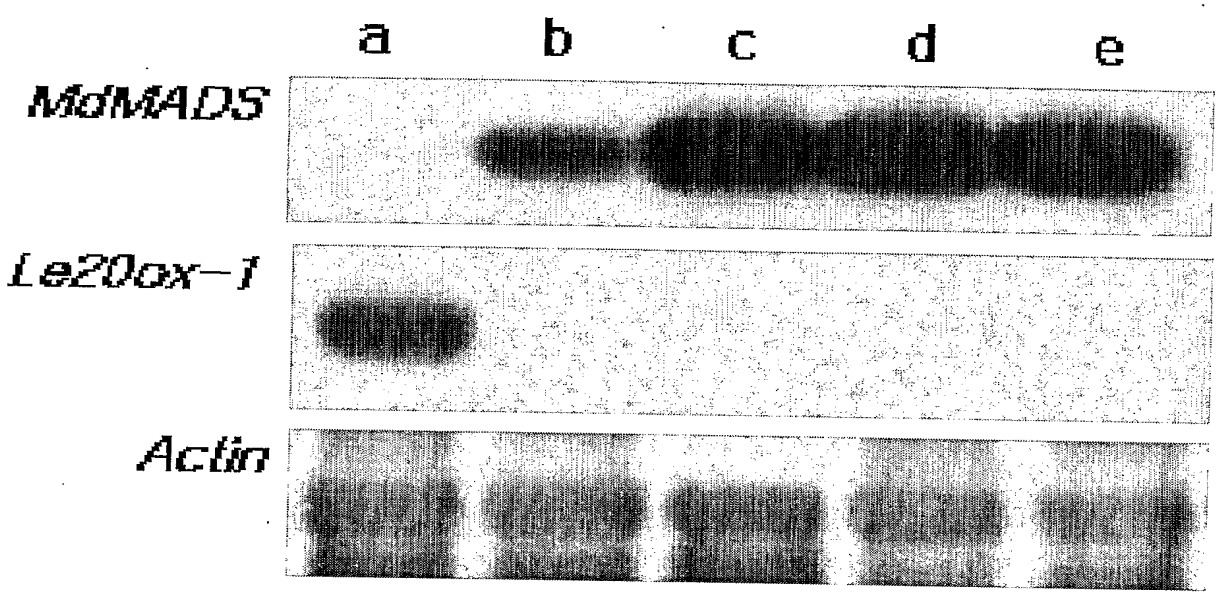

FIG. 19